

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/121,017B
Source: 1FW16
Date Processed by STIC: 11/29/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER:

09/121,017B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ✓ PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.** *Suggestion: download PatentIn 3.4 from USPTO website*

1,3,5,17,19, ←
21,23,25,27,29
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFW16

RAW SEQUENCE LISTING

DATE: 11/29/2006

PATENT APPLICATION: US/09/121,017B

TIME: 13:50:37

Input Set : A:\sequence listing final.txt

Output Set: N:\CRF4\11292006\I121017B.raw

*Does Not Comply
Corrected Diskette Needed*

see pp 1, 3-4, 6

5 <110> APPLICANT: Imamura, Toru

7 Asada, Masahiro

9 Oka, Syuichi

11 Suzuki, Masashi

13 Yoneda, Atsuko

15 Ota, Keiko

17 Oda, Yuko

19 Miyakawa, Kazuko

21 Orikasa, Noriko

23 Asada, Chie

25 Kojima, Tetsuhito

29 <120> TITLE OF INVENTION: HEPARIN-BINDING PROTEINS MODIFIED WITH SUGAR CHAINS,

31 METHOD OF PRODUCING THE SAME AND PHARMACEUTICAL

33 COMPOSITIONS CONTAINING THE SAME

37 <130> FILE REFERENCE: 382.1019

41 <140> CURRENT APPLICATION NUMBER: 09/121,017B

43 <141> CURRENT FILING DATE: 1998-07-22

47 <150> PRIOR APPLICATION NUMBER: 307721/1997

49 <151> PRIOR FILING DATE: 1997-11-10

53 <160> NUMBER OF SEQ ID NOS: 31

57 <170> SOFTWARE: PatentIn Ver. 2.0

61 <210> SEQ ID NO: 1

63 <211> LENGTH: 221

65 <212> TYPE: PRT

67 <213> ORGANISM: Artificial Sequence

W--> 71 <220> FEATURE:

W--> 71 <223> OTHER INFORMATION:

W--> 71 <400> 1

73 Met Ala Pro Ala Arg Leu Phe Ala Leu Leu Phe Phe Val Gly Gly

75 1 5 10 15

79 Val Ala Glu Ser Ile Arg Glu Thr Glu Val Ile Asp Pro Gln Asp Leu

81 20 25 30

85 Leu Glu Gly Arg Tyr Phe Ser Gly Ala Leu Pro Asp Asp Glu Asp Val

87 35 40 45

91 Val Gly Pro Gly Gln Glu Ser Asp Asp Phe Glu Leu Ser Gly Ser Gly

93 50 55 60

97 Asp Leu Asp Asp Leu Glu Asp Ser Met Ile Gly Pro Glu Val Val His

99 65 70 75 80

103 Pro Leu Val Pro Leu Asp Ala Asn Tyr Lys Lys Pro Lys Leu Leu Tyr

105 85 90 95

109 Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val

111 100 105 110

115 Asp Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser

*suggestion: download PatentIn 3.4
from www.uspto.gov (USPTO
website)*

*see p.6 and item 6 on Error
summary
sheet*

RAW SEQUENCE LISTING

DATE: 11/29/2006

PATENT APPLICATION: US/09/121,017B

TIME: 13:50:37

Input Set : A:\sequence listing final.txt

Output Set: N:\CRF4\11292006\I121017B.raw

```

117          115          120          125
121 Ala Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln
123          130          135          140
127 Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro
129 145          150          155          160
133 Asn Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn
135          165          170          175
139 Thr Tyr Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu
141          180          185          190
145 Lys Lys Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr Gly Gln
147          195          200          205
151 Lys Ala Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp
153          210          215          220
159 <210> SEQ ID NO: 2
161 <211> LENGTH: 663
163 <212> TYPE: DNA
165 <213> ORGANISM: Artificial Sequence
169 <220> FEATURE:
171 <223> OTHER INFORMATION: Description of Artificial Sequence: fusion of
173      sequence for a part of human rydocal and a part of human fibroblast
175      growth factor 1
179 <220> FEATURE:
181 <221> NAME/KEY: CDS
183 <222> LOCATION: (1)..(663)
187 <400> SEQUENCE: 2
189 atg gcc ccc gcc cgt ctg ttc gcg ctg ctg ctg ttc ttc gta ggc gga 48
191 Met Ala Pro Ala Arg Leu Phe Ala Leu Leu Leu Phe Phe Val Gly Gly
193 1 5 10 15
197 gtc gcc gag tcg atc cga gag act gag gtc atc gac ccc cag gac ctc 96
199 Val Ala Glu Ser Ile Arg Glu Thr Glu Val Ile Asp Pro Gln Asp Leu
201 20 25 30
205 cta gaa ggc cga tac ttc tcc gga gcc cta cca gac gat gag gat gta 144
207 Leu Glu Gly Arg Tyr Phe Ser Gly Ala Leu Pro Asp Asp Glu Asp Val
209 35 40 45
213 gtg ggg ccc ggg cag gaa tct gat gac ttt gag ctg tct ggc tct gga 192
215 Val Gly Pro Gly Gln Glu Ser Asp Asp Phe Glu Leu Ser Gly Ser Gly
217 50 55 60
221 gat ctg gat gac ttg gaa gac tcc atg atc ggc cct gaa gtt gtc cat 240
223 Asp Leu Asp Asp Leu Glu Asp Ser Met Ile Gly Pro Glu Val Val His
225 65 70 75 80
229 ccc ttg gtg cct cta gat gct aat tac aag ccc aaa ctc ctc tac 288
231 Pro Leu Val Pro Leu Asp Ala Asn Tyr Lys Lys Pro Lys Leu Leu Tyr
233 85 90 95
237 tgt agc aac ggg ggc cac ttc ctg agg atc ctt ccg gat ggc aca gtg 336
239 Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val
241 100 105 110
245 gat ggg aca agg gac agg agc gac cag cac att cag ctg cag ctc agt 384
247 Asp Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser
249 115 120 125

```

RAW SEQUENCE LISTING

DATE: 11/29/2006

PATENT APPLICATION: US/09/121,017B

TIME: 13:50:37

Input Set : A:\sequence listing final.txt

Output Set: N:\CRF4\11292006\I121017B.raw

```

253 gcg gaa agc gtg ggg gag gtg tat ata aag agt acc gag act ggc cag 432
255 Ala Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln
257 130 135 140
261 tac ttg gcc atg gac acc gac ggg ctt tta tac ggc tca cag aca cca 480
263 Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro
265 145 150 155 160
269 aat gag gaa tgt ttg ttc ctg gaa agg ctg gag gag aac cat tac aac 528
271 Asn Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn
273 165 170 175
277 acc tat ata tcc aag aag cat gca gag aag aat tgg ttt gtt ggc ctc 576
279 Thr Tyr Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu
281 180 185 190
285 aag aag aat ggg agc tgc aaa cgc ggt cct cgg act cac tat ggc cag 624
287 Lys Lys Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr Gly Gln
289 195 200 205
293 aaa gca atc ttg ttt ctc ccc ctg cca gtc tct tct gat 663
295 Lys Ala Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp
297 210 215 220

```

303 <210> SEQ ID NO: 3

305 <211> LENGTH: 175

307 <212> TYPE: PRT

309 <213> ORGANISM: Artificial Sequence

W--> 313 <220> FEATURE:

W--> 313 <223> OTHER INFORMATION:

W--> 313 <400> 3

```

315 Met Ser Arg Gly Ala Gly Arg Val Gln Gly Thr Leu Gln Ala Leu Val
317 1 5 10 15
321 Phe Leu Gly Val Leu Val Gly Met Val Val Pro Ser Pro Ala Gly Ala
323 20 25 30
327 Arg Ala Asn Gly Thr Leu Leu Asp Ala Asn Tyr Lys Lys Pro Lys Leu
329 35 40 45
333 Leu Tyr Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly
335 50 55 60
339 Thr Val Asp Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln
341 65 70 75 80
345 Leu Ser Ala Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr
347 85 90 95
351 Gly Gln Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln
353 100 105 110
357 Thr Pro Asn Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His
359 115 120 125
363 Tyr Asn Thr Tyr Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val
365 130 135 140
369 Gly Leu Lys Lys Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr
371 145 150 155 160
375 Gly Gln Lys Ala Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp
377 165 170 175

```

381 <210> SEQ ID NO: 4

383 <211> LENGTH: 525

see p.6 and Error Summary Sheet

RAW SEQUENCE LISTING

DATE: 11/29/2006

PATENT APPLICATION: US/09/121,017B

TIME: 13:50:38

Input Set : A:\sequence listing final.txt

Output Set: N:\CRF4\11292006\I121017B.raw

```

385 <212> TYPE: DNA
387 <213> ORGANISM: Artificial Sequence
391 <220> FEATURE:
393 <223> OTHER INFORMATION: Description of Artificial Sequence: fusion of
395     sequence for a part of mouse fibroblast growth factor 6 and
397     a part of human fibroblast growth factor 1
401 <220> FEATURE:
403 <221> NAME/KEY: CDS
405 <222> LOCATION: (1)..(525)
409 <400> SEQUENCE: 4
411 atg tcc cgg gga gca gga cgt gtt cag ggc acg ctg cag gct ctc gtc 48
413 Met Ser Arg Gly Ala Gly Arg Val Gln Gly Thr Leu Gln Ala Leu Val
415 1 5 10 15
419 ttc tta ggc gtc cta gtg ggc atg gtg gtg ccc tca cct gcc ggc gcc 96
421 Phe Leu Gly Val Leu Val Gly Met Val Val Pro Ser Pro Ala Gly Ala
423 20 25 30
427 cgc gcc aac ggc acg cta ctg gac gct aat tac aag aag ccc aaa ctc 144
429 Arg Ala Asn Gly Thr Leu Leu Asp Ala Asn Tyr Lys Lys Pro Lys Leu
431 35 40 45
435 ctc tac tgt agc aac ggg ggc cac ttc ctg agg atc ctt ccg gat ggc 192
437 Leu Tyr Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly
439 50 55 60
443 aca gtg gat ggg aca agg gac agg agc gac cag cac att cag ctg cag 240
445 Thr Val Asp Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln
447 65 70 75 80
451 ctc agt gcg gaa agc gtg ggg gag gtg tat ata aag agt acc gag act 288
453 Leu Ser Ala Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr
455 85 90 95
459 ggc cag tac ttg gcc atg gac acc gac ggg ctt tta tac ggc tca cag 336
461 Gly Gln Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln
463 100 105 110
467 aca cca aat gag gaa tgt ttg ttc ctg gaa agg ctg gag gag aac cat 384
469 Thr Pro Asn Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His
471 115 120 125
475 tac aac acc tat ata tcc aag aag cat gca gag aag aat tgg ttt gtt 432
477 Tyr Asn Thr Tyr Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val
479 130 135 140
483 ggc ctc aag aag aat ggg agc tgc aaa cgc ggt cct cgg act cac tat 480
485 Gly Leu Lys Lys Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr
487 145 150 155 160
491 ggc cag aaa gca atc ttg ttt ctc ccc ctg cca gtc tct tct gat 525
493 Gly Gln Lys Ala Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp
495 165 170 175
503 <210> SEQ ID NO: 5
505 <211> LENGTH: 181
507 <212> TYPE: PRT
509 <213> ORGANISM: Artificial Sequence
W--> 513 <220> FEATURE:
W--> 513 <223> OTHER INFORMATION:

```

*see p.6 and item 6 on
Error Summary
Sheet*

*This type of error
appears in subsequent
sequences*

RAW SEQUENCE LISTING

DATE: 11/29/2006

PATENT APPLICATION: US/09/121,017B

TIME: 13:50:38

Input Set : A:\sequence listing final.txt

Output Set: N:\CRF4\11292006\I121017B.raw

W--> 513 <400> 5

```

515 Met Ser Arg Gly Ala Gly Arg Val Gln Gly Thr Leu Gln Ala Leu Val
517   1           5           10           15
521 Phe Leu Gly Val Leu Val Gly Met Val Val Pro Ser Pro Ala Gly Ala
523           20           25           30
527 Arg Ala Gln Gly Thr Leu Leu Asp Ala Asn Tyr Lys Lys Pro Lys Leu
529           35           40           45
533 Leu Tyr Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly
535   50           55           60
539 Thr Val Asp Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln
541  65           70           75           80
545 Leu Ser Ala Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr
547           85           90           95
551 Gly Gln Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln
553           100          105          110
557 Thr Pro Asn Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Ala Ala
559           115          120          125
563 Thr Pro Ala Pro Asn His Tyr Asn Thr Tyr Ile Ser Lys Lys His Ala
565           130          135          140
569 Glu Lys Asn Trp Phe Val Gly Leu Lys Lys Asn Gly Ser Cys Lys Arg
571 145           150          155          160
575 Gly Pro Arg Thr His Tyr Gly Gln Lys Ala Ile Leu Phe Leu Pro Leu
577           165          170          175
581 Pro Val Ser Ser Asp
583           180

```

589 <210> SEQ ID NO: 6

591 <211> LENGTH: 543

593 <212> TYPE: DNA

595 <213> ORGANISM: Artificial Sequence

599 <220> FEATURE:

```

601 <223> OTHER INFORMATION: Description of Artificial Sequence: fusion of
603     sequence for a part of mouse fibroblast growth factor 6,
605     a part of human fibroblast growth factor 1 and an artificial
607     sequence

```

611 <220> FEATURE:

613 <221> NAME/KEY: CDS

615 <222> LOCATION: (1)..(543)

619 <400> SEQUENCE: 6

```

621 atg tcc cgg gga gca gga cgt gtt cag ggc acg ctg cag gct ctc gtc   48
623 Met Ser Arg Gly Ala Gly Arg Val Gln Gly Thr Leu Gln Ala Leu Val
625   1           5           10           15
629 ttc tta ggc gtc cta gtg ggc atg gtg gtg ccc tca cct gcc ggc gcc   96
631 Phe Leu Gly Val Leu Val Gly Met Val Val Pro Ser Pro Ala Gly Ala
633           20           25           30
637 cgc gcc caa ggc acg cta ctg gac gct aat tac aag aag ccc aaa ctc   144
639 Arg Ala Gln Gly Thr Leu Leu Asp Ala Asn Tyr Lys Lys Pro Lys Leu
641           35           40           45
645 ctc tac tgt agc aac ggg ggc cac ttc ctg agg atc ctt ccg gat ggc   192
647 Leu Tyr Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly

```

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 11/29/2006
PATENT APPLICATION: US/09/121,017B TIME: 13:50:39

Input Set : A:\sequence listing final.txt
Output Set: N:\CRF4\11292006\I121017B.raw

Use of <220> Feature(NEW RULES):

Sequence(s) __ are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"
or "Unknown". Please explain source of genetic material in <220> to <223>
section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32)
(Sec.1.823 of new Rules)

Seq#:1,3,5,17,19,21,23,25,27,29

VERIFICATION SUMMARY

DATE: 11/29/2006

PATENT APPLICATION: US/09/121,017B

TIME: 13:50:39

Input Set : A:\sequence listing final.txt

Output Set: N:\CRF4\11292006\I121017B.raw

L:71 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:1, <213>
ORGANISM:Artificial Sequence
L:71 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:1, <213>
ORGANISM:Artificial Sequence
L:71 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:71
L:313 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:3, <213>
ORGANISM:Artificial Sequence
L:313 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:3, <213>
ORGANISM:Artificial Sequence
L:313 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:313
L:513 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:5, <213>
ORGANISM:Artificial Sequence
L:513 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:5, <213>
ORGANISM:Artificial Sequence
L:513 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:513
L:973 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:17, <213>
ORGANISM:Artificial Sequence
L:973 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:17, <213>
ORGANISM:Artificial Sequence
L:973 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:17,Line#:973
L:1201 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:19, <213>
ORGANISM:Artificial Sequence
L:1201 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:19, <213>
ORGANISM:Artificial Sequence
L:1201 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:19,Line#:1201
L:1431 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:21, <213>
ORGANISM:Artificial Sequence
L:1431 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:21, <213>
ORGANISM:Artificial Sequence
L:1431 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:21,Line#:1431
L:1701 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:23, <213>
ORGANISM:Artificial Sequence
L:1701 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:23, <213>
ORGANISM:Artificial Sequence
L:1701 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:23,Line#:1701
L:1999 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:25, <213>
ORGANISM:Artificial Sequence
L:1999 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:25, <213>
ORGANISM:Artificial Sequence
L:1999 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:25,Line#:1999
L:2199 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:27, <213>
ORGANISM:Artificial Sequence
L:2199 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:27, <213>
ORGANISM:Artificial Sequence
L:2199 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:27,Line#:2199
L:2441 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:29, <213>
ORGANISM:Artificial Sequence
L:2441 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:29, <213>
ORGANISM:Artificial Sequence
L:2441 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:29,Line#:2441